

04 FEB 2003

9303414

PCT/EP 03/08549

# BUNDESREPUBLIK DEUTSCHLAND



REC'D 03 OCT 2003

WIPO

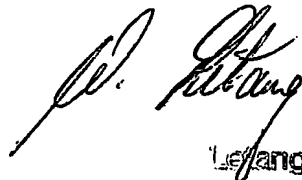
PCT

## Prioritätsbescheinigung über die Einreichung einer Patentanmeldung

**Aktenzeichen:** 102 36 001.4  
**Anmeldetag:** 06. August 2002  
**Anmelder/Inhaber:** Icon Genetics AG,  
München/DE  
**Bezeichnung:** Plastid Transformation Using Modular Vectors  
**IPC:** C 12 N 15/82

Die angehefteten Stücke sind eine richtige und genaue Wiedergabe der ursprünglichen Unterlagen dieser Patentanmeldung.

München, den 04. September 2003  
Deutsches Patent- und Markenamt  
Der Präsident  
Im Auftrag



Leifang

**PRIORITY DOCUMENT**  
SUBMITTED OR TRANSMITTED IN  
COMPLIANCE WITH  
RULE 17.1(a) OR (b)

**BEST AVAILABLE COPY**

## Plastid Transformation Using Modular Vectors

### FIELD OF INVENTION FIELD OF INVENTION

The present invention relates to plant biotechnology in general and more particularly to a process and vectors for plastid transformation of plants. Specifically, the present invention provides a process of genetic transformation of plant plastids, vectors for the process, and plants or plant cells obtained or obtainable according to the process of the invention.

### BACKGROUND OF THE INVENTION

According to generally accepted knowledge, two classes of cell organelles, i.e. plastids and mitochondria, are derived from initially independent prokaryotes that were taken up into a predecessor of present day eukaryotic cells by separate endosymbiotic events (Gray, 1991). As a consequence, these organelles contain their own DNA, DNA transcripts in the form of messenger RNA, ribosomes, and at least some of the necessary tRNAs that are required for decoding of genetic information (Marechal-Drouard et al., 1991).

While, shortly after endosymbiotic uptake, these organelles were genetically autonomous since they contained all the elements necessary to drive prokaryotic life, this autonomy was reduced during evolution by transfer of genetic information to the cell's nucleus. Nevertheless, their genetic information is of sufficient complexity to make recent cell organelles an attractive target for gene technology. This is particularly the case with plastids, because these organelles still encode about 50% of the proteins required for their main function inside the plant cell, photosynthesis. Plastids also encode their ribosomal RNAs, the majority of their tRNAs and ribosomal proteins. In total, the number of genes in the plastome is in the range of 120 (Palmer, 1991). The vast majority of proteins that are found in plastids are, however, imported from the nuclear/cytosolic genetic compartment.

#### *Plastids can be genetically transformed*

With the development of general molecular cloning technologies, it became soon possible to genetically modify higher plants by transformation. The main emphasis in plant transformation was and still is on nuclear transformation, since the majority of genes, ca. 26.000 in the case of *Arabidopsis thaliana*, the complete sequence of which was recently published (The Arabidopsis Genome Initiative, 2000), is found in the cell's nucleus. Nuclear transformation was easier to achieve, since biological vectors such as *Agrobacterium tumefaciens* were available, which could be modified to efficiently enable nuclear

transformation (Galvin, 1998). In addition, the nucleus is more directly accessible to foreign nucleic acids, while the organelles are surrounded by two envelope membranes that are, generally speaking, not permeable to macromolecules such as DNA.

A capability of transforming plastids is highly desirable since it could make use of the high gene dosage in these organelles that bears the potential of extremely high expression levels of transgenes. In addition, plastid transformation is attractive because plastid-encoded traits are not pollen transmissible; hence, potential risks of inadvertent transgene escape to wild relatives of transgenic plants are largely reduced. Other potential advantages of plastid transformation include the feasibility of simultaneous expression of multiple genes as a polycistronic unit and the elimination of positional effects and gene silencing that may result following nuclear transformation.

Methods that allow stable transformation of plastids could indeed be developed for higher plants. To date, two different methods are available, i.e. particle bombardment of tissues, in particular leaf tissues (Svab et al., 1990), and treatment of protoplasts with polyethylene glycol (PEG) in the presence of suitable transformation vectors (Koop et al., 1996). Both methods mediate the transfer of plasmid DNA across the two envelope membranes into the organelle's stroma.

Conventional methods for plastid transformation usually rely on the selection for the insertion of an antibiotic resistance marker cassette into the plastome such as an expression cassette containing the gene *aadA* (encoding the enzyme aminoglycoside adenyl transferase), which confers resistance to inhibitors like Spectinomycin or Streptomycin (US5877402) or *aphA-6* (encoding the enzyme aminoglycoside phosphotransferase A-6), which confers resistance to Kanamycin (Huang et al., 2002). Alternatively selection is achieved by replacing a complete resident plastid gene by a mutant gene, which confers resistance to selection inhibitors (US5451513). These selection marker genes that are needed for the selection of transgenic plant cells from a vast background of untransformed cells and code for antibiotic or herbicide resistance genes. The selection marker gene or the mutant plastid gene is included in the integrating region, which is flanked by homologous regions directing the plastome integration. Selection for plastid transformants is then achieved by cultivating transformed plant material on medium containing the appropriate inhibitor. As these marker genes are stably integrated into the genome together with the genes of interest, they will remain in the homoplastomic transgenic plants although they are not required for the function of the genes of interest. These remaining marker genes are a main issue of criticism of plant biotechnology. Construction of a selection system which does not result in a resistance gene in the transgenic plant is, therefore, highly desirable (Iamtham and Day, 2000).

Conventional plastid transformation technology is described in Heifetz, 2000 and Koop et al.,

1996.

Plastid transformation vectors usually contain one or more gene(s) of interest flanked by two regions of the insertion site, which are necessary for the stable introduction of the engineered sequences into the plastome by homologous recombination events (US5877402, US5451513). However, a substantial cloning work is needed to generate the transformation vector molecules, which consist of a large number of different fragments: two flanks, a marker gene, one or more gene(s) of interest and regulatory elements such as promoter, 5'-UTR, 3'-UTR or spacer elements.

The cloning of transformation vectors is problematic in cases, in which (at least one of) the cloned gene(s) has a toxic effect on the bacteria used for cloning. Moreover, using the highly desirable potential to co-express a series of introduced transgenes is limited by the overall size of the transforming plasmid.

One major complication in achieving plastid transformation is the high copy number of the plastome. Following transfer of the vector DNA into the plastids only one or very few copies of the introduced molecules will recombine with the plastome. Thus initially only a small proportion of recombinant plastome molecules are generated in the background of a vast majority of wild type plastome molecules ("heteroplastomic status"). By a very time consuming process of segregation under selective pressure it is possible to eliminate the original wild type copies of the plastome and achieve a "homoplastomic recombinant status", being characterized by the sole presence of recombinant plastome molecules. Achieving the homoplastomic status is supported by several cycles of regeneration on selective medium containing the appropriate antibiotics. Usually 3 - 5 of such cycles are necessary to obtain the homoplastomic recombinant status. The presence of remaining copies of wild type plastome can be monitored by molecular analysis like PCR or Southern Hybridization. As several weeks are needed for one regeneration cycle it takes several months to generate homoplastomic plastid transformants.

Therefore, it is an object of the invention to provide a novel, efficient, rapid and highly versatile process of genetic transformation of plant plastids, whereby genetically stable transgenic plants or plant cells may be produced.

It is another object of the invention to provide a process of genetic transformation of plant plastids, which allows a significant reduction of the number of regenerations cycles needed to achieve homoplastomic plants.

It is another object of the invention to provide a process of genetic transformation of plant plastids, which allows expression of multiple genes of interest (polycistronic expression).

It is a further object to provide vectors, which can be used in a modular fashion thus reducing the cloning work and the overall size of the plasmid molecules.

It is a further object to provide vectors which allow the cloning of sequences having toxic

effects on the bacteria used for cloning.

It is a further object to provide a method that allows the generation of transformants which do not carry a resistance marker gene in the final plant or plant cell.

## GENERAL DESCRIPTION OF THE INVENTION

The above objects are achieved by the process of claim 1. Preferred embodiments are defined by the subclaims.

It has been surprisingly found that it is possible to generate transgenic plants or plant cells transformed on their plastomes by introducing into plant plastids at least two DNA molecules containing overlapping sequences, which results in a continuous integration sequence in the final transplastomic plant. The process of the invention features several important advantages over conventional plastid transformation processes. These advantages are given below.

The process of the invention comprises introducing a first and a second DNA molecule into plastids of a plant to be transformed. These DNA molecules which are used as vectors may be introduced consecutively, i.e. in two separated steps, or simultaneously, i.e. in a one-step procedure. It is less laborious and therefore preferred to introduce said two DNA molecules in a one-step procedure, e.g. by using a mixture of said DNA molecules. For introducing said DNA molecules, known transformation methods may be used (see below).

The design of said two DNA molecules is of central importance for the process of the invention. Said first DNA molecule contains a first region homologous to a region of the plastome for directing plastome integration and a first sequence of interest. Said second DNA molecule contains a second region homologous to a region of the plastome for directing plastome integration and a second sequence of interest. Thus, one region homologous to a region of the plastome is sufficient for each DNA molecule. Preferably, said first or said second DNA molecule contains only one region homologous to a region of the plastome for directing plastome integration. More preferably, said first and said second DNA molecule both contain only one region homologous to a region of the plastome for directing plastome integration.

Said homologous regions direct integration of each DNA molecule to a desired site of the plastome. The first and the second homologous together determine the type of DNA modification (e.g. insertion, deletion) of the plastome by the process of the invention. In a preferred embodiment, the aim of performing the process of the invention is to introduce an integration sequence into the plastome without any further plastome modification like a deletion of plastome sequences. Preferably, said homologous regions of the first and the second DNA molecules correspond together to a continuous plastome sequence. Generally, said

homologous regions are derived from plastomes of the plant species to be transformed. As long as sufficient homology for homologous recombination is guaranteed, the homologous regions may be derived from other plant species, preferably however, from closely related plant species.

The length of each homologous region for plastome integration may vary in a wide range as long as the recombination frequency is sufficient. Each homologous region may have a length of between 100 and 5000 bp. Usually, the recombination frequency decreases as the length of the homologous regions decreases. Therefore the length is preferably at least 200 to 300 bp. More preferably, the length is between 500 and 2000 bp, most preferably between 500 and 1000 bp.

Said sequences of interest may contain any nucleotide sequence to be integrated into the plastome. As typical example, said sequences of interest contain a gene to be expressed. Said first and said second sequence of interest may each contain a fragment of a gene to be expressed, whereby said gene is assembled in said integration sequence. The invention is highly versatile in this respect. Preferably, however, said first and said second sequence of interest are different.

Said first sequence of interest contains a sequence segment that is homologous to a sequence segment of said second sequence of interest. Thus, this homologous segment is an overlapping region of said first and said second sequence of interest. The homologous sequence segment allows recombination of said first and said second sequence of interest such that an integration sequence is formed in the plastome, whereby said integration sequence contains at least a portion of said first and at least a portion of said second sequence of interest as a continuous sequence. The sequence segment in a sequence of interest is preferably positioned at the distal end of the sequence of interest with respect to said homologous region that directs plastome integration.

As a minimum requirement, said first and said second sequence of interest each contains said homologous sequence segment, i.e. a sequence that of sufficient homology to enable homologous recombination between said first and said second sequence of interest. Preferably, the homologous sequence segment of the first and of the second sequence of interest are identical.

Said first and said second sequence of interest may be identical, leading to an integration sequence consisting of said sequence of interest. In this limiting case, each sequence of interest may be considered to consist of said homologous sequence segment. This limiting case is not a preferred case of the invention. Preferably, said first or said second sequence of interest contains a sequence in addition to said homologous sequence segment. More preferably, said first and said second sequence of interest each contains a sequence in

addition to said homologous sequence segment, whereby said additional sequences in said first and said second sequence of interest are different.

Recombination between said overlapping regions (homologous sequence segments) of the vectors can take place inside the plastome to form said integration sequence. Said integration sequence preferably comprises sequence portions from said first and from said second sequence of interest. If said first and said second sequence of interest each contains a gene of interest, an integration sequence may be formed comprising two genes of interest. Thus, the process of the invention may be used for assembling a desired integration sequence from said first and said second sequence of interest. The assembly of the integration sequence may be used to generate in the plastids a new function not present in one of said sequences of interest alone. As an example, a gene of interest consisting of a coding sequence and of various regulatory sequences may be assembled to a functional form in said integration sequence. Further, a coding sequence of interest in said first sequence of interest may be combined with a promoter or other regulatory sequences provided with said second sequence of interest (or vice versa). In this way, a regulatory sequence giving rise to a desired expression of said coding sequence may be selected or screened for.

The process of the invention may comprise introducing one or more additional DNA molecules into said plant plastids in addition to said first and said second DNA molecule. Said additional DNA molecule(s) comprise(s) additional sequence(s) of interest. If a third DNA molecule is introduced, said third DNA molecule preferably contains a sequence segment homologous to a sequence segment of said first sequence of interest and a sequence segment homologous to said second sequence of interest. Said third DNA molecule does preferably not have a homologous region for plastome integration.

After transformation, transformants are selected that contain the desired integration sequence. Selection is typically supported by an inhibitor or antibiotic the transformants are resistant against due to a marker gene. Selection may further comprise allowing segregation of transformed and untransformed sectors (e.g. on leaves). Transformants or transformed sectors may be identified by molecular analysis, e.g. PCR and Southern blotting. Further, transformants or transformed sectors may be identified phenotypically, e.g. by the expression of a transgene. A transgene may e.g. be detected by Western blotting, by a characteristic enzymatic activity or by another characteristic property like optical, notably fluorescent property.

A marker gene for selecting transformants may be introduced into a plastome with said first or said second sequence of interest. As noted above, a marker gene may also be introduced as fragments with said first and said second sequence of interest and combined to a functional form in said integration sequence. An important embodiment of the process of the

invention allows to produce marker free transplastomic plants. This may be achieved by including a selectable marker gene in one of said DNA molecules outside of a sequence unit consisting: of said region homologous to a region of the plastome and said sequence of interest. Such a positioning of a marker gene allows loss of said marker gene in the course of recombination events that take place. A selectable marker gene may be included in said first or said second DNA molecule in the described fashion, or in said first and said second DNA molecule. The positioning of said marker gene outside of said sequence unit results in excision of the marker gene out of the plastome in the course of recombination events envisaged in this invention, making amenable marker free transplastomic plants. It is obvious to the skilled person, that the inhibitor or antibiotic for the used marker gene is applied only transiently in the selection of step (b). At a later stage, the antibiotic is left out from the medium in order to allow loss of the marker gene(s) by homologous recombination events mediated by duplicated sequences, which have been generated during vector integration

In a specific embodiment of the process of producing marker free transplastomic plants, a selectable marker gene is split into a first and a second fragment, whereby said first fragment is incorporated in said first DNA molecule outside of a first sequence unit and said second fragment is incorporated in said second DNA molecule outside of a second sequence unit. Said first sequence unit consists of said first homologous region and said first sequence of interest. Said second sequence unit consists of said second homologous region and said second sequence of interest.

The process of the invention may be applied to all plants. Preferably, it is applied to multi-cellular plants. Most preferably, the process of the invention is applied to crop plants. Examples of crop plants are given in the definitions.

The invention further provides a kit-of-parts comprising a first and a second DNA molecule as defined herein. The invention further provides a DNA molecule for plastid transformation containing one region homologous to a region of a plastome for directing plastome integration and a sequence of interest. Further, a library of DNA molecules as defined herein is provided, whereby each of said DNA molecules contains a different sequence of interest. Also, plants or plant cells transformed with said DNA molecules of said kit-of-parts or with said DNA molecule of the invention is provided.

#### *Advantages of the process of the invention*

The process described herein may be applied to introduce sequences of interest such as genes or regulatory elements or to introduce mutations such as point mutations insertions or deletions into the plastome.



The process of the invention allows to generate transplastomic plants, whereby the homoplastomic state can be attained after less regeneration cycles than with prior art processes. Depending on the particular embodiment, homoplastomic plants may be achieved after 0 to 4 regeneration cycles, preferably after 2 cycles, and more preferably after 1 regeneration cycle. In special embodiments, the homoplastomic state is achieved in primary transformants without a regeneration cycle. Thus, the process of the invention allows an enormous reduction of the time required to achieve homoplastomic transplastomic plants. The reasons for this surprising efficiency improvement is presently unclear. Compared to conventional plastid transformation the method described herein is faster, because fewer steps are necessary to obtain homoplastomic plants.

The method allows the use of smaller transformation vectors, for which cloning is simpler than in the case of conventional plastid transformation vectors.

The method relieves plastid transformation from any limitation on the number or size of sequences to be introduced, because an unlimited number of transformation vectors with overlapping sequences may be used.

The method relieves plastid transformation from any limitation imposed by sequences, which are toxic for the bacteria used for cloning, because the toxic sequences may be cloned into two different vector molecules in a way that each of them separately can not be toxic, even if they are expressed into a protein sequence.

Moreover the method described herein allows the use of combinatorial vector libraries, whereby the vectors of the library contain different sequences of interest.

The method can be applied to generate transformants, whereby the final plant does not carry any resistance marker gene.

Any of the above mentioned aspects of this new method offers substantial advantage compared to conventional plastid transformation. Taken together the process and vectors of this invention constitute an enormous progress on both speed, usability and flexibility of plastid transformation in general.

## DEFINITIONS

- 3'-UTR:** transcribed but not translated region of a (->) **gene**, downstream of a (->) **coding region**;
- 5'-UTR:** transcribed but not translated region of a (->) **gene**, upstream of a (->) **coding region**; in (->) **plastid (->) genes**, the **5'-UTR** contains sequence information for translation initiation (ribosome binding site, (->) **RBS**) close to its 3' end;

- aadA:** (->) **coding region** of bacterial aminoglycoside adenylyl transferase, a frequently used protein, that detoxifies antibiotic (->) **selection inhibitors** spectinomycin and/or streptomycin;
- aphA-6** (->) **coding region** of bacterial aminoglycoside phosphotransferase A-6, a protein that detoxifies the antibiotic (->) **selection inhibitor:** kanamycin
- chloroplast:** (->) **plastid** containing chlorophyll;
- coding region:** nucleotide sequence containing the information for a) the amino acid sequence of a polypeptide or b) the nucleotides of a functional RNA; coding regions are optionally interrupted by one or more (->) **intron(s)**;
- flank, flanking region:** DNA sequences at the 5' and 3' ends of inserts in a conventional (->) **plastid** (->) **transformation** (->) **vector**, which mediate integration into the target (->) **plastome** of sequences between the flanks by double reciprocal (->) **homologous recombination**. By the same mechanism, sequences can be modified or removed from the target (->) **plastome**. Thus, the flanks of the (->) **plastid** (->) **transformation** (->) **vector** determine, where changes in the target (->) **plastome** are generated by (->) **transformation**;
- gene expression:** process turning sequence information into function; in (->) **genes** encoding polypeptides, gene expression requires the activity of a (->) **promoter**, which initiates and directs RNA polymerase activity, leading to the formation of a messenger RNA, which is subsequently translated into a polypeptide; in (->) **genes** encoding RNA, the (->) **promoter**-mediated activity of RNA polymerase generates the encoded RNA;
- gene(s):** nucleotide sequence(s) encoding all elements, which are required to secure function e.g. expression independently;
- genes are organised in (->) **operons**, which contain at least one complete (->) **coding region**; in (->) **genes** encoding polypeptides, these elements are: (1) a (->) **promoter**, (2) a 5' untranslated region ((->) **5'-UTR**), (3) a complete (->) **coding region**, (4) a 3' untranslated region ((->) **3'-UTR**); in (->) **genes** encoding RNA, the (->) **5'-UTR** and the (->) **3'-UTR** are missing; in (->) **operons** consisting of more than one (->) **coding region**, two subsequent complete (->) **coding regions** are separated by a (->) **spacer**, and

	(->) <b>promoter</b> , (->) <b>5'-UTR</b> , and (->) <b>3'-UTR</b> elements are shared by the (->) <b>coding regions</b> of that (->) <b>operon</b> ;
<b>gene of interest:</b>	modified or newly introduced sequence: the purpose of a (->) <b>transformation attempt</b> ;
<b>genome:</b>	Complete DNA sequence of a cell's nucleus or a cell organelle;
<b>GFP</b>	green fluorescent protein
<b>homologous recombination:</b>	process leading to exchange, insertion or deletion of sequences due to the presence of one or more (->) <b>flanks</b> with sufficient sequence homology to a target site in a (->) <b>genome</b> ;
<b>intron:</b>	sequence interrupting a (->) <b>coding region</b> ;
<b>operon:</b>	organisational structure of several (->) <b>genes</b> sharing a promoter;
<b>plant(s):</b>	organism(s) that contain(s) (->) <b>plastids</b> in its (their) cells; this invention particularly relates to multicellular (->) <b>plants</b> ; these include the group of gymnosperms (such as pine, spruce and fir etc.) and angiosperms (such as the <i>monocotyledonous</i> crops maize, wheat, barley, rice, rye, Triticale, sorghum, sugar cane, asparagus, garlic, palm tress etc., and non-crop monocots, and the <i>dicotyledonous</i> crops tobacco, potato, tomato, rape seed, sugar beet, squash, cucumber, melon, pepper, Citrus species, egg plant, grapes, sunflower, soybean, alfalfa, cotton etc.), and no-crop dicots as well as ferns, liverworths, mosses, and multicellular green, red and brown algae;
<b>plastid(s):</b>	organelle(s) with their own genetic machinery in (->) <b>plant</b> cells, occurring in various functionally and morphologically different forms, e.g. amyloplasts, (->) <b>chloroplasts</b> , chromoplasts, etioplasts, gerontoplasts, leukoplasts, proplastids etc;
<b>plastome:</b>	complete DNA sequence of the (->) <b>plastid</b> ;
<b>promoter:</b>	nucleotide sequence functional in initiating and regulating transcription;
<b>RBS, ribosomal binding site:</b>	DNA sequence element upstream of the (->) <b>translation start codon</b> of a (->) <b>coding region</b> , that mediates ribosome binding and translation initiation from the respective RNA transcript; <b>RBS</b> elements are either part of (->) <b>5'-UTRs</b> or of (->) <b>spacers</b> ;
<b>selection inhibitor:</b>	chemical compound, that reduces growth and development of non-transformed cells or organelles stronger than that of transformed ones;

<b>sequence of interest</b>	modified or newly introduced sequence of any length: the purpose of a (->) <b>transformation</b> attempt; if introduction of a sequence is not intended, the length of the sequence of interest can be zero, i.e. it can be of interest not to have a sequence of interest. In the present invention, a sequence of interest of a DNA molecule used as a vector has at least one sequence segment homologous to a sequence segment of another DNA molecule used as a vector.
<b>transformation vector:</b>	cloned DNA molecule that was generated to mediate (->) <b>transformation</b> of a (->) <b>genome</b> ;
<b>transformation:</b>	process leading to the introduction, the excision or the modification of DNA sequences by treatment of (->) <b>plants</b> or plant cells including the use of at least one (->) <b>transformation vector</b> ;
<b>transgene:</b>	DNA sequence derived from one (->) <b>genome</b> , introduced into another one;
<b>uidA:</b>	(->) <b>coding region</b> of bacterial $\beta$ glucuronidase, a frequently used reporter protein.

## SHORT DESCRIPTION OF THE FIGURES

**Figure 1** Simplified scheme of recombination events in conventional plastid transformation: The integration of transformation vector sequences into the plastome takes place by two homologous recombination events mediated by two homologous flanks. The corresponding wild type region from the plastome is transferred to the plasmid vector.

**Figure 2** Suggested model of recombination events in conventional plastid transformation based on our observations: the first homologous recombination via the left or the right flank leads to the transient (reversible) insertion of the whole transformation vector generating a duplication of the respective flanking sequence. A second homologous recombination via the right or the left flank, respectively, leads to the excision of the duplicated sequences. The corresponding wild type region from the plastome is transferred to the plasmid vector.

**Figure 3** PCR analysis of tobacco transformants transformed with pKCZ after up to three regeneration cycles (reference example). Gel A (cycle 0), Gel B (cycle I), Gel C (cycle II) and Gel D (cycle III) show the products obtained using primers oSH3 and oSH58 which are specific

for detecting complete pKCZ integration. Gel E, illustrates that with the primer combination oFCH60 and oSH58 all the cycle-III lines still contain the *aadA* selection cassette even though not all carry complete vector insertion events (cf. example 1).

**Figure 4** Suggested model of recombination events by using modular vectors according to the invention (vector 1 and vector 2). The first integration step is shown for either vector 1 or vector 2. The following second integration step is shown only for vector 1 (on the right) into a plastome region already containing vector 2. The second integration step of vector 2 into a plastome region already containing vector 1 (not shown) proceeds in an analogous fashion. After full vector integration of both vectors, the final transformed plastome (bottom) is obtained by deletion events of homologous repetitive elements.

**Figure 5** Scheme showing the homologous region of vector 1 (hpr 1) and of vector 2 (hpr 2) for directing plastome integration by homologous recombination. hpr stands for homologous plastome region. Further, the sequence of interest in both vectors is shown (white boxes plus vertically hatched box). The vertically hatched boxes (designated olr for overlapping region) represents a sequence segment of said first sequence of interest (soi) that is homologous to a sequence segment of said second sequence of interest (soi). These homologous sequence segments or overlapping regions allow recombination of vector 2 and vector 1 in the plastome. Within the sequences of interest, the homologous sequence segments are preferably positioned distal to the hpr sequences. At the bottom, the obtained transplastome containing the integration sequence is shown.

**Figure 6** Scheme showing the use of a further vector (vector 3) in addition to said first and said second vector of the invention. Vector 3 does not have to contain a homologous region for plastome integration. Vector 3 has two homologous segments or overlapping regions (vertically hatched boxes). One overlapping region (olr1) shares homology with a homologous sequence segment of vector 1. The other overlapping region (olr2) shares homology with a homologous sequence segment of vector 2. olr1 and olr2 are preferably non identical. hpr, homologous plastome region; soi, sequence of interest; olr, overlapping region.

**Figure 7** Scheme showing the production of marker free transplastomic plants. Vector 2 contains a selectable marker gene outside of the sequence unit consisting of the homologous

region and the sequence of interest. Integration of vector 1 and vector 2 leads to the transplastome after insertion of vector 1 and 2, that may be selected by transiently applying the suitable antibiotic. Recombination via the duplicated elements leads to excision of sequences including the marker gene. hpr, homologous plastome region; soi, sequence of interest; olr, overlapping region.

**Figure 8** Conventional plastid transformation vector pKCZ. aadA, aminoglycoside adenyl transferase; INSL, *N. tabacum* plastome sequence from bp 131106-132277; INSR, *N. tabacum* plastome sequence from bp 132278-133396; AP<sup>r</sup>,  $\beta$ -lactamase.

**Figure 9** Modular plastid transformation vector pICF742. aadA, coding sequence for aminoglycoside adenyl transferase; LpsbA, 5'-UTR from *N. tabacum* psbA gene; Prpl32, promoter from *N. tabacum* rpl32 gene; INSR, *N. tabacum* plastome sequence from bp 132279-133390; AP<sup>r</sup>,  $\beta$ -lactamase.

**Figure 10** Modular plastid transformation vector pICF743. aadA, coding sequence for aminoglycoside adenyl transferase; Talpha, alpha operon terminator from *E. coli*; INSL, *N. tabacum* plastome sequence from bp 131106-132277; AP<sup>r</sup>,  $\beta$ -lactamase

**Figure 11** Primer binding sites for PCR analysis of tobacco transformants from cotransformation of pICF742 and pICF743. A, primer pair A; B, primer pair B; C, primer pair C.

**Figure 12** PCR analysis of tobacco transformants from cotransformation of pICF742 and pICF743. 1, line 1; 2, line 2, A, primer pair A; B, primer pair B; C, primer pair C; left three lanes, control without DNA.

**Figure 13** Southern blot of tobacco transformants from cotransformation of pICF742 and pICF743. A and C, restriction with Bsp120I; B, restriction with AccIII. 1-5, line 1-5; M, marker lane (from top: 10 kb, 8 kb, 6 kb, 5 kb, 4 kb, 3 kb, 2.5 kb, 1.5 kb, 1 kb); WT, wild type control.

## DETAILED DESCRIPTION AND PREFERRED EMBODIMENTS

*When using conventional plastid transformation vectors, a high number of regeneration cycles is required to achieve homoplastomic transformants*

Conventional plastid transformation vectors usually contain an integration sequence, which is not present in the wild type plant consisting of a selectable marker gene, one or more gene(s) of interest and regulatory elements such as promoters, 5'-UTRs, 3'-UTRs or spacer elements. In the vector, the integration sequence is flanked by two sequences homologous to the targeting plastome thus directing the position of the plastome integration. Insertion of the integration region into the target plastome is achieved by double reciprocal homologous recombination events. A simplified model suggests that integration occurs via two homologous recombination events, one event at each flank (Fig. 1). However, the actual molecular process is difficult to monitor and may be more complex involving intermediates. Experimental data obtained in our laboratory suggest that a first recombination event mediated by one of the two flanks leads to the integration of the full transformation vector, thus duplicating the flanking sequence (Fig. 2). Indeed, integration of the whole circular plasmid vector could be demonstrated by PCR and Southern Hybridization analysis (Fig. 3). At a different point in time a second recombination event can either cause a reversion of the first integration. Alternatively a second recombination between the two other duplicated flanking sequences causes excision of both the plasmid backbone and the duplicated fragments leaving the integrating sequence in the plastome (Fig. 2).

Using conventional plastid transformation vectors it takes several months to achieve homoplastomic plastid transformants, because up to 5 cycles of regeneration are necessary. A certain number of cell generations is required to convert the heteroplastomic cells into homoplastomic cells by segregation. Segregation into the desired configuration of the plastomes is driven by applying selective conditions.

*The vectors of this invention contain not more than one homologous region*

In contrast to conventional plastid transformation methods this invention discloses a process for producing transplastomic plants or plant cells, in which at least two different types of DNA molecules (e.g. transformation vectors) are introduced into plastids, preferably simultaneously. One homologous region for directing plastome integration is sufficient for each of said vectors, preferably each vector contains not more than one homologous region for

directing plastome integration. Further, each vector contains a sequence of interest that is preferably not present in the wild type plant. The sequences of interest of said vectors will result in an integration sequence in the transplastomic plant obtained.

The integration sequence may contain foreign genes such as a marker gene or other sequences of interest. The marker gene may be any gene conferring resistance against an inhibitor such as an antibiotic resistance gene like *aphA-6* or an herbicide resistance gene like *bar* or an visible marker gene like GFP.

Examples for other sequences of interest are any genes encoding or capable of expressing a useful protein like proinsulin, interferone, human serum albumin, human growth factors, peptides functioning as vaccines (such as a vaccine against hepatitis B) or genes for technical enzymes. However, the integration sequence to be generated may also consist in a deletion of plastid sequences, e.g. in order to generate specific mutants.

In the process of the invention, at least two DNA molecules (e.g. vectors) are released into the plastid, each containing a homologous region defining the integration site of the plastome. Preferably, said first or said second DNA molecule does not have more than one homologous region for directing plastome integration. More preferably, neither said first nor said second DNA molecule has more than one homologous region for directing plastome integration. This does not exclude the use of elements in the sequences of interest that have homology to plastome sequences like promoters or regulatory elements or other plastid sequences. If such elements homologous to plastid sequences are used in the a sequence of interest, they may in principle also act as plastome integration sequences leading to undesired integration events. Such undesired integration events may in many cases be unproblematic, e.g. if they do not lead to stable transformants or to transformants that may be selected for by the selectable marker employed. Moreover, undesired transformants may be detected by molecular analysis e.g. of the integration sequence.

Elements homologous to plastid sequences are preferably significantly shorter than the homologous regions for plastome integration. This measure generally achieves a significantly lower recombination frequency for said homologous elements than for said homologous regions. Alternatively, such elements homologous to plastid sequences are preferably taken from plastome sequences located far away from the desired integration site of the DNA molecule to impede undesired recombination events.

The at least two different vector molecules are either released simultaneously or in two or more different transformation steps. Simultaneous transformation of at least two types of



molecules is called co-transformation. Following co-transformation of the at least two vector molecules, the first regenerates containing plastids with the desired plastome modification appear after about 3 weeks of cultivation under adequate selection and culture conditions, depending on the transformation method applied. The method of co-transformation can be used with any transformation method which is suitable for generation of plastid transformants. Examples for suitable plastid transformation methods are the biolistic transformation, the PEG-mediated transformation, other transfection methods using chemical agents or the electric field mediated transfection of nucleic acids.

Alternatively, the at least two vector molecules may be applied in separated transformation steps. Consecutive transformation by at least two transformation steps leads to the same integration results observed during co-transformation.

If a third vector is used in addition to said first and said second DNA molecule, the third vector does not have to contain any homologous sequences derived from the target plastome, as long as the sequences of interest of the vectors contain an overlapping region sufficient for recombination. The same is true if more than three vectors are used.

Fragments of the marker gene may be located on different vectors, whereby the marker gene is assembled by recombination processes.

*The vectors of this invention enable the generation of homoplastomic plants in a very short time*

Surprisingly it was found that using the method described herein it is possible to recover homoplastomic plastid transformants after only two cycles of regeneration. Preferably, even one regeneration cycle is sufficient. In many cases, the regenerates recovered after transforming plant tissue or plant cells are homoplastomic even without any regeneration cycle being performed. In contrast to conventional plastid transformation vectors it is possible to obtain homoplastomic plants after a very short period of only several weeks. Therefore, the invention described herein offers an enormous acceleration of the process and a drastic reduction of the work needed for tissue culture.

Homoplastomic transformants do not contain any wild type plastomes. The presence of wild type plastomes can be monitored by methods such as Southern hybridization or PCR analysis. In transplastomic plant material recovered from primary regenerates which appear after transformation of plant tissue or cells, routine Southern analysis was performed to identify recombinant plastomes and to detect remaining wild type plastomes. 40 % of the analyzed material from these primary regenerated does not contain any remaining wild type plastomes.

Wild type plastomes could be eliminated from the other regenerates in only one step of sub-culture, whereas up to 5 cycles of sub-culture are needed using conventional transformation vectors.

A hypothetical mechanism for the introduction of foreign sequences according to this invention is described in figure 4. According to this model, one of the two vector molecules which contain a homologous region recombine with the respective plastome sequence. The homologous recombination event leads to the integration of the whole vector including the plasmid backbone. It also leads to a duplication of the homologous region. This process is reversible and may result in an excision of the recombinant sequence by homologous recombination mediated by the duplicated homologous regions unless the process is stabilized by another integration event. If the integration sequence contains a selectable marker gene which can be expressed, the vector will tend to stay integrated if selective pressure is applied. In the absence of any selective pressure, the plastome with one integrated vector is highly unstable. A second recombination event however may lead to the integration of at least one other molecule. If the other molecule contains another homologous region, a recombination with the respective homologous region of the plastome may occur. Alternatively, it is also possible that the recombination is mediated by any of the other repeated sequences such as the vector backbone or the overlapping region of the molecules. The second recombination event may occur between the free first vector and the integrated second vector (shown in fig. 4), or between the free second vector and the integrated first vector (not shown in fig. 4) or between the integrated first vector and the integrated second vector located on different plastome molecules (not shown in fig. 4). Vector molecules that do not contain a homologous plastid region may only recombine with the other repeated sequences. In either case, an integration of the whole second vector molecule will appear. In cases where more than two vector molecules are used, all the molecules will integrate by one of the homologous regions. After integration of the different molecules into the plastome, a vast series of secondary intramolecular recombinations between any of the repeated sequences is possible. As a consequence all the repeated regions will be eliminated. The final result of these various recombination events is the generation of a continuous recombinant region referred to as integration sequence.

*The vectors of this invention can be used in a combinatorial approach*

Expression in plastids is useful for a broad range of different purposes ranging from modified nutrient composition to high level expression of pharmaceuticals in plants. For that

purpose it is necessary to obtain a set of interchangeable promoters and regulatory elements differing in strength and expression pattern. This allows to construct expression vectors for different purposes (weak, strong, constitutive or regulated expression etc.). The elements should be interchangeable to modify the expression level. For many cases it is favourable to use promoters, 5'-UTR and 3'-UTR from different genes because this excludes internal recombinations where the inserted gene is exchanged with an endogenous gene via identical 5'- and 3'-UTRs. On the other hand, 5'- and 3'-UTRs sometimes interact and together determine translation activities. It is therefore not always possible to estimate the effect of a particular combination. Modular vectors of this invention containing only the 5'- or 3'-regulatory elements allow an easy and fast way of combining different regulatory elements thus generating the desired expression cassette in the integration sequence. Vectors with different elements can be kept in libraries and can be combined at will. Moreover, if the optimal combination of different elements is not known, a mixture of different regulatory elements on different vectors can be used for transformation. The expression cassette with the desired properties is then obtained by selection of the transformant with desired properties, optionally followed by molecular analysis.

*The vectors of this invention avoid surplus cloning work*

Conventional plastid transformation vectors usually contain a selectable marker gene needed for the selection of the transformants, one or more gene(s) of interest and regulatory elements such as promoters, 5'-UTRs, 3'-UTRs or spacer elements. It needs a substantial effort to generate these highly complex plasmids consisting of many different elements. However, in different transformation vectors many identical elements are used. Using the method of this invention it is possible to construct a vector that contains these identical elements, such as a homologous region, a selection marker gene and regulatory elements in one molecule. The at least one other transformation vector carries the different sequences of interest to be introduced into the plastome. Combining the first vector molecule with any other adequate vector containing any of the desired sequences reduces the complexity of the plasmids and consequently the effort to construct these molecules.

*The vectors of this invention are smaller than conventional plastid transformation vectors and thus allow for the insertion of more sequences of interest*

Construction of transformation vectors is frequently restricted by insert size limitations. Conventional plastid transformation vectors usually contain two homologous regions, a selectable marker and regulatory elements. Therefore, only a limited number of additional sequences can be introduced. However it may be desirable to engineer complex metabolic pathways in the plastids, which depend on the expression of several different enzymes. As the vectors of the invention contain less compulsory sequences compared to conventional vectors, it is possible to insert longer sequences of interest. In addition, more than two transformation vectors with overlapping regions may be used in order to introduce even larger integration sequences which are assembled in the plastids.

*The vectors of this invention avoid problems derived from toxic effects of some sequences on the bacteria used for cloning*

Genetic engineering can use the potential of plants as self-reproducible factories for the production of a vast number of organic substances. It has been shown, that an economic and environmentally friendly production of substances like enzymes, diagnostics or therapeutics in plants is possible.

In some cases however, the genes to be introduced into plants can have toxic effects on the bacteria used for cloning. In these cases, construction of the transformation vector is restricted. An example for a sequence that has toxic effects on bacteria is the gene HbsAg encoding a surface antigen of the Hepatitis B virus. Expression of the gene in plant plastids would be desirable, because it would constitute a source for a vaccine e.g. against Hepatitis. However cloning of the full gene including the regulatory elements used in conventional transformation vectors is restricted, because the plastid regulatory elements are also active in bacteria. Using the vectors of this invention it is possible to split the full expression cassette of a gene like HbsAg between two molecules in a way that none of the vectors alone contains an expressible cassette. Using that approach the restrictive effects of genes toxic for bacteria are overcome.

*The vectors of this invention allow the generation of resistance marker free plants*

A method for obtaining plastid transformants which are devoid of resistance marker genes is highly desirable in order to prevent unwanted spread of the marker gene into the environment. Conventional plastid transformation vectors usually contain a suitable resistance marker gene which is necessary for the selection of the transformants. The resistance marker

is located in the integration sequence of the transformation vector and leads to a stable plastome integration of the resistance gene in the final plant.

Using the process and vectors described in this invention it is possible to place such resistance marker genes outside the sequence unit consisting of the homologous region and the sequence of interest. Following transformation an integration of the full transformation vector occurs (fig. 2), which leads to the transient insertion of the selection marker in the plastome. The recombination event causes a duplication of the homologous region. Transformed cells can be selected for on a medium containing the appropriate inhibitor during that stage. As soon as the plant material is transferred to inhibitor-free medium, the selective pressure for the maintenance of the full vector integration is released. Further recombination events (as described in figure 4) mediated by the previously generated duplicated homologous regions lead to an excision of the selection marker gene. Consequently, the final plant does not carry the resistance marker gene used for selection of the transformants.

The resistance marker gene may also be split in two or more overlapping fragments, each located on a different vector, whereby the resistance is only mediated if the fragments recombine to the complete expressible marker gene.

Preferred embodiments of the invention are now described in detail.

#### *Embodiment 1: Co-transformation of two vectors*

Plastids are transformed simultaneously with said first and said second DNA molecule referred to as modular vectors (fig 5). Vector 1 (said first DNA molecule) contains one region homologous to a plastome region (said first homologous region). The integration of sequences of interest should take place downstream of this plastome region. The homologous region typically has a length of 500 to 1000 bp. If desirable, shorter or longer sequences may also be used. On vector 1, the first sequence of interest is located downstream of this homologous region. The upstream part of the integration sequence is contained in the first sequence of interest downstream of this homologous region.

Vector 2 (said second DNA molecule) contains one region homologous to a plastome region (said second homologous region). The integration of sequences of interest should take place upstream of this plastome region. The homologous region typically has a length of 500 to 1000 bp, too. On vector 2, the second sequence of interest is located upstream of this homologous region. The downstream part of the integration sequence is contained in the second sequence of interest upstream of this homologous region.

In this preferred embodiment, the two homologous regions of the two vectors are present next to each other on the plastome without intervening sequences. A sequence segment of the downstream region of the first sequence of interest on vector 1 is homologous to a sequence segment of the upstream region of the second sequence of interest on vector 2. This homologous sequence segment is also referred to as overlapping region. Typically, this homologous sequence segment has a length of 500 to 1000 bp. After the recombination events described in the invention, the cotransformation of the two vectors results in a continuous integration sequence integrated between the two plastome regions used as homologous regions. Typically, each vector only contains a part of the integration sequence.

It has been shown that recombination also takes place with longer or shorter homologous regions, but a length of 500 to 1000 bp is sufficient for efficient recombination and can be amplified easily with standard PCR procedures.

The marker gene for selecting transformants can be located as two fragments on the two vectors, i.e. one fragment on each vector. The marker gene may be split into two fragments in several ways. Non limiting examples for that splitting are:

- a) The promoter and 5'-UTR are located on vector 1. The coding sequence is located on the overlapping region of vector 1 and vector 2. The 3'-UTR is located on vector 2.
- b) The promoter, 5'-UTR and 5'-part of the coding sequence are located on vector 1. The middle part of the coding sequence is located on the overlapping region of vector 1 and vector 2. The 3'-part of the coding sequence and the 3'-UTR are located on vector 2.

If the homologous regions on the vectors are chosen such that the integration sequence is integrated in a plastome region transcribed by an endogenous promoter, it is not necessary to include a promoter in front of the marker gene. Besides the marker gene, additional gene(s) of interest may be included either in the sequences of interest of vector 1 or vector 2 or both.

#### *Embodiment 2: Co-transformation of fragmented genes on two vectors*

Since plastids and bacteria have similar expression systems, it is sometimes difficult or even impossible to clone plastid transformation vectors in *E. coli*, if genes are involved the gene products of which are toxic for *E. coli*. This problem is solved by splitting such a gene into 2 or more fragments as described for the marker gene in embodiment 1. On each vector, the toxic gene is then present as an incomplete gene or fragment that is non toxic. Plastids are then transformed simultaneously with two modular vectors as described in embodiment 1, whereupon the functional complete gene of interest is reassembled within the plastids.

### *Embodiment 3 Co-transformation of three vectors*

For some purposes it is advantageous to distribute an integration sequence necessary for stable plastid transformation on three vectors (fig. 6). Non limiting examples are: insertion of very long integration sequences (e.g. gene clusters), serial construction of transformation vectors etc .

Vector 1 contains a first region homologous to the plastome region and a first sequence of interest downstream thereof. The integration of the integration sequence should take place downstream of this plastome region. Downstream of the first homologous region, the upstream part of the integration sequence is present in the first sequence of interest.

Vector 2 contains a second region homologous to the plastome region and a second sequence of interest. The integration of the integration sequence should take place upstream of this plastome region. Upstream of this homologous region, the downstream part of the integration sequence is present in the second sequence of interest. As described for embodiment 1, the homologous sequences are typically 500 to 1000 bp long, but are not limited to this length.

Vector 3 contains a third sequence of interest, the upstream part of which is homologous to the sequence of interest of vector 1 and the downstream part is homologous to a sequence of interest of vector 2. Vector 3 may or may not contain the complete integration sequence which should be integrated into the plastome.

### *Embodiment 4: marker-free transplastomic plants*

If the marker gene is located outside of the region designed for integration, the marker gene will be present in the full vector integration intermediates (fig. 7). When selection pressure is released, the marker gene is excised together with vector sequences. The homologous plastid sequences and sequences of interest are arranged as described in embodiment 1. Contrary to embodiment 1, the marker gene is not included in the sequence of interest. Instead it is located elsewhere on vector 1 or vector 2. Preferably, the marker gene is separated from the unit consisting of the homologous region and the sequence of interest by vector sequences. Preferably, vector 1 and vector 2 each contains a marker gene in this fashion, whereby these marker genes are different, e.g. *aadA* and *aphA6*. Selection is then carried out by using a combination of the two respective antibiotics e.g 500 mg/l spectinomycin + 25 mg/l kanamycin. Alternatively, a fragment of a marker gene is located on vector 1 and the other fragment of the marker gene is located on vector 2, whereby both fragments are outside the above-defined unit.

It is a prerequisite then that both fragments share a homologous segment (overlapping region) which allows recombination of both fragments to assemble a complete functional marker gene after insertion of both vectors into the plastome. As only a fraction of the possible recombination events yields a functional marker, the selection pressure maintains intermediates containing said functional marker. When selection pressure is removed, the marker gene together with remaining vector sequences will be removed by recombination due to repetitive vector sequences.



## Examples

Molecular biology methods used in this invention are well known in the art and are described for example by Sambrook et al. (1989) Molecular cloning and by Ausubel et al. (1999) Short protocols in Molecular Biology.

### **Example 1:** PCR analysis of complete vector integration (via one flank) into the plastid genome

#### Plastid transformation vector pKCZ

pKCZ is a conventional plastid transformation vector where the selection marker is cloned between the two flanks used for homologous recombination. The vector is designed to make a neutral insertion between *trnR* and *trnN* in the inverted repeat region of the tobacco plastid genome (Zou, 2001). pKCZ comprises two flanking sequences for homologous recombination (corresponding to *Nicotiana tabacum* plastome sequences 31106-132277 and 132278-133396, according to GenBank accession number Z00044) and an *aadA* plastid expression cassette under control of the 16s rRNA promoter (Koop et al., 1996). A schematic drawing of the plasmid construct is shown in figure 8.

#### Generation of primary transformants and subsequent selection for homoplastomic lines

Particle gun-mediated plastid transformation and subsequent selection were carried out as described in Mühlbauer et al, 2002. Selection of transformants was based on the resistance to the antibiotics spectinomycin/streptomycin, conferred by the *aadA* gene product. In order to simplify transformed plastid genomes and to eliminate wild-type genomes, the primary transformants (cycle-0) were subjected to several additional rounds of regeneration (from small leaf explants) on selective media containing spectinomycin (here designated as cycle-I, cycle-II etc).

#### Analysis of primary transformants by PCR

Plastid transformants (cycle-0) were identified by PCR using total DNA isolated with the DNeasy Plant Mini Kit (QIAGEN, Hilden, Germany). To determine the presence of the *aadA* gene the primers oSH81 (5'-CTATCAGAGGTAGTTGGCGTC-3') and oFCH60 (5'-CACTACATTTGCTCATCGCC-3') were used. The PCR program was as follows: 3 min at 94 °C, 1 cycle; 45 sec at 94 °C, 45 sec at 55 °C, 2 min at 72°C, 30 cycles; final extension at 72°C

for 10 min. The results showed that 48 lines from 54 analysed (6 bombarded leaves) gave the expected amplification product of 504 bp. To prove correct integration of the *aadA* cassette within the tobacco plastome primers oSH58 (5'-TATTCCGACTTCCCCAGAGC-3') and oFCH60 (5'-CACTACATTTGCTCATCGCC-3') were used. Primer oSH58 is located outside (downstream) of the right flank of pKCZ in the tobacco plastome and in combination with oFCH60 can only give the expected product of 2106 bp upon integration of the *aadA* expression cassette between *trnR* and *trnN* in the inverted repeat. The PCR program was as follows: 5 min at 94 °C, 1 cycle; 45 sec at 94 °C, 45 sec at 55 °C, 3.5 min at 72°C, 35 cycles; final extension at 72°C for 7 min. All 48 of the *aadA* PCR positive lines showed the expected right-flank-*aadA* product of 2106 bp.

Ten of the cycle-0 transformants (1:1, 1:2, 1:3, 1:4, 1:5, 2:1, 2:4, 2:5 2:6 and 2:7) were selected for further analysis.

#### PCR analysis of transformants containing completely integrated vectors

Normally, the production of stable plastid transformants is thought to occur via two simultaneous recombination events occurring between the left and right flanks of the transforming molecule and the plastome (as depicted in figure 1). An alternative mechanism is presented in figure 2. Here, complete integration of the vector occurs first, via recombination with one flank only (either left or right) with the plastome, resulting in the generation of a hypothetical unstable intermediate. Subsequent additional recombination events can then take place between the duplicated flanks in this molecule to generate either the wild-type situation or a stably integrated *aadA* cassette. In order to test for this possibility, PCR was performed using primers oSH3 (5'-GGCATCAGAGCAGATTG-3') and oSH58 (5'-TATTCCGACTTCCCCAGAGC-3'). Primer oSH3 is located within the vector backbone of pKCZ (pUC18) and primer oSH58 is located outside (downstream) of the right flank of pKCZ in the tobacco plastome. A product of 2638 bp can only be obtained with these two primers when complete pKCZ integration has occurred as shown in figure 2. No PCR product of the expected size will be obtained from the wild type plastome fragment (comprising left and right flanks) since the binding site for oSH3 is absent. The PCR program was as follows: 5 min at 94 °C, 1 cycle; 45 sec at 94 °C, 45 sec at 55 °C, 3.5 min at 72°C, 35 cycles; final extension at 72°C for 7 min. Nine of the 10 cycle-0 transformants analysed showed a PCR product of 2.6 kb which would be consistent with complete integration of pKCZ into the plastid genome within these lines (fig. 3A). No product of the correct size was observed in the wild type control or in sample

1:1. Since complete integration of pKCZ results in the formation of an unstable intermediate it is to be expected that with increasing time additional recombination events between the duplicated flanks in this molecule will lead to either the wild-type situation or a stably integrated *aadA* cassette. As such DNA samples prepared from cycle-I and cycle-II plant material were analysed by PCR with primers oSH3 and oSH58. If the model presented in fig. 2 is correct the probability of amplifying the 2638 bp band with primers oSH3 and oSH58 should be reduced with each regeneration cycle on selection. The results suggest that this is indeed the case since only 5 of the 10 cycle-I lines analysed gave a strong PCR product of the expected size (fig. 3B). Furthermore, in cycle-II the number of lines showing clear amplification of the expected 2638 bp band was further reduced.

The model presented in figure 2 also predicts that all cycle-II lines which are negative for complete vector integration should still show PCR signals consistent with a stably integrated *aadA* cassette due to the molecular rearrangements previously described. To prove integration of the *aadA* cassette within the tobacco plastome primers oSH58 (5'-TATTCGACTTCCCCAGAGC-3') and oFCH60 (5'-CACTACATTCGCTCATCGCC-3') were used. The PCR program was as follows: 5 min at 94 °C, 1 cycle; 45 sec at 94 °C, 45 sec at 55 °C, 3.5 min at 72°C, 35 cycles; final extension at 72°C for 7 min. All 10 of the cycle-II transformants show the expected right-flank-*aadA* product of 2106 bp (fig. 3D) which would be consistent with the scenario shown in figure 2.

## Example 2 Construction of overlapping modular vectors

Modular vector pICF742 (fig. 9) consists of the right flanking region homologous to the tobacco plastome, the tobacco *rpl32* promoter, the tobacco *psbA*-5'-UTR and the *aadA* marker gene.

The right flanking region was amplified from tobacco plastid DNA (bp 132279 to bp 133390 of the *N. tabacum* plastome) with modifying primers 5'-TGGAGCTCGAATTGCCGCGAGCAAAGATATTAATG-3' and 5'-TACGAATTCAAGAGAAGGTCACGGCGAGAC-3', introducing an *SacI* recognition site at the 5'-end and an *EcoRI* recognition site at the 3'-end. The PCR product was purified and digested with *SacI* and *EcoRI* and ligated into a pUC18 plasmid which was digested with the same enzymes. The *rpl32* promoter was amplified from tobacco plastid DNA (bp 113917 to bp 114055 of the *N. tabacum* plastome) with modifying primers 5'-GACCCTGCAGGCAAAAATCTCAAATAGCC-3' and 5'-CGGGATCCGATTTTCTTTAGACTTCGG-3', introducing a *PstI* recognition site at

the 5'-end and a BamHI recognition site at the 3'-end. The PCR product was reamplified with modifying primers 5'- CGGGATCCGATTTTTCTTTAGACTTCGG-3' and 5'- CGAGCTCCACCGCGGTGGCGGCCCGTCGACCCTGCAGGCAAAAATCTC-3' to introduce a new multi cloning site containing a SacI recognition site at the 5'-end. The resulting PCR product was digested with BamHI and SacI and ligated into the similar restricted pUC18 vector containing the right flanking region. The psbA-5'-UTR was amplified from tobacco plastid DNA (complementary to bp 1598 - bp 1680 of the *N. tabacum* plastome) with modifying primers 5'- C G G G A T C C A A A A G C C T T C C A T T T T C T A T T T - 3 ' and 5 ' - TTGCAGCCATGGTAAAATCTTGGTTTATT-3' introducing a BamHI recognition site at the 5'-end and a NcoI recognition site at the 3'-end. The PCR product was digested with NcoI and BamHI. The aadA sequence from *E. coli* was amplified from plasmid pFaadAll (Koop et al., 1996) with the modifying primer 5'- TGAATTCCCATGGCTCGTGAAGCGG-3' and 5'- GGTGATGATGATCCTTGCCAACTACCTTAGTGATCTC-3' introducing a NcoI recognition site at the 5'-end. The PCR product was reamplified with primers 5'- T G A A T T C C C A T G G C T C G T G A A G C G G - 3 ' and 5 ' - GCTCTAGATTAGTGATGATGGTGATGATGATCCTTGCC-3' to introduce a His-tag and XbaI recognition site at the 3'-end. The PCR product was digested with NcoI and XbaI. The pUC18 vector containing the right flanking region and the rpl32 promoter was digested with BamHI and XbaI and ligated with the digested psbA-5'-UTR and the digested aadA. The resulting plasmid was digested with XbaI and NdeI to remove the remaining pUC18 multicloning site. The digested plasmid was purified on an agarose gel. The band at 4600 bp was extracted purified and the ends filled in with Klenow polymerase. The plasmid was then relegated, resulting in pICF742. Modular vector pICF743 (fig 10) consists of the left flanking region homologous to the tobacco plastome, the alpha operon terminator from *E. coli* and the aadA marker gene.

The multicloning site of pUC18 between PaeI and SapI was removed and replaced by a new multicloning site consisting of (from 5' to 3') BamHI, KpnI, XbaI and NcoI. The left flanking region was amplified from tobacco plastid DNA (bp 131106 to bp 132277 of the *N. tabacum* plastome) with modifying primers 5'- GATGGATCCTTGCTGTTGCATCGAAAGAG -3' and 5'- CACTGGTACCCGGAATTGTGACCTCTCGGGAGAATC -3', introducing a BamHI recognition site at the 5'-end and a KpnI recognition site at the 3'-end. The PCR product was purified and digested with BamHI and KpnI and ligated into the pUC18 plasmid with new multicloning site, which was digested with the same enzymes. The resulting plasmid was digested with KpnI and XbaI. The digested vector was ligated with the single strand oligonucleotide 5'-

GATGTCTAGAAGCAACGTAAAAAACCCGCCCCGGCGGGTTTTTTTATACCCGTAGTATCCCCAGCGGCCG CCGTAC-3', coding for the *E. coli* alpha operon terminator. The complementary strand was filled in with Taq polymerase, digested with XbaI and religated. The resulting vector was digested with NcoI and XbaI and ligated with the *aadA* PCR product from pICF742, resulting in vector pICF743.

12.5 µg of vector pICF742 and 12.5 µg of vector pICF743 were mixed, loaded on gold particles and transformed in *N. tabacum* plastids by particle bombardement as described in Mühlbauer et al, 2002. Selection of transformants was based on the resistance to the antibiotics spectinomycin/streptomycin, conferred by the *aadA* gene product. In order to amplify transformed plastid genomes and to eliminate wild-type genomes, the primary transformants (cycle-0) were subjected to several additional rounds of regeneration (from small leaf explants) on selective media containing spectinomycin (here designated as cycle-I, cycle-II etc).

Two spectinomycin/streptomycin resistant calli from cycle-0 were analysed by PCR to verify the transformation. Three different primer pairs were used (fig. 11):

- A) 5'-CAGACTAATACCAATCCAAGCC-3' (binding outside the left flanking region at the *N. tabacum* plastome) and 5'-CTATCAGAGGTAGTTGGCGTC-3' (binding at the marker gene).
- B) 5'-CACTACATTTTCGCTCATCGCC-3' (binding at the marker gene) and 5'-TATTCCGACTTCCCCAGAGC-3' (binding outside the right flanking region at the *N. tabacum* plastome)
- C) 5'-CATCAATACCTCGGTCTAG-3' (binding at the left flanking region) and 5'-ACACATAGTATGCCCGGTC-3' (binding at the right flanking region).

PCR with all three primer showed amplicates, proving the integration of both vectors resulting in one continuous integrated region (fig. 12). The calculated amplicate sizes are 2139 bp (A), 2035 bp (B) and 1450 bp (C) which fits well with the observed sizes. Remarkably no wild type signal (290 bp) is visible with primer pair C, indicating that even in such an early stage no untransformed is present.

Five spectinomycin/streptomycin resistant calli from cycle-0 and cycle-I were then analysed in three independent Southern blot experiments (fig. 13). Two lines showed the presence of solely the complete correct integrated *aadA* gene (line 1 and line 3: 3.8 kb for Bsp120I restriction and 6.7 kb for AccIII restriction). One line (line 2) showed the integrated *aadA* gene and an additional signal (4.9 kb for Bsp120I restriction and 3.5 kb for AccIII restriction) corresponding to an intermediate recombination. Two lines (line 4 and line 5) showed the intermediate recombination signal (4.9 kb for Bsp120I restriction) and the wild type signal (2.6 kb for Bsp120I

restriction). This result indicates that 2 out of the 5 analysed lines reached the homoplastomic integration status within very short time

### References:

Koop et al., 1996, *Planta* 199, 193-201

Galvin S. B., 1998, *Curr. Opin. Biotechnol.*, 9, 227-232.

Gray M. W., Origin and Evolution of Plastid Genomes and Genes, in: Bogorad L. and Vasil I. K. (eds.), *Cell Culture and Somatic Cell Genetics of Plants*, Volume 7A, Academic Press, San Diego, 1991.

Heifetz, P., 2000, *Biochimie*, 82, 655-666.

Huang F.-C., Klaus S., Herz S., Koop H.-U., Golds T., 2002, *MGG*, in press.

Iamtham and Day, 2000, *Nat. Biotechnol.*, 18, 1172-1176.

Marechal-Drouard L., Kuntz M., Weil J. H., tRNAs and tRNA Genes of Plastids, in: Bogorad L. and Vasil I. K. (eds.), *Cell Culture and Somatic Cell Genetics of Plants*, Volume 7A, Academic Press, San Diego, 1991.

Mühlbauer S., Lössl A., Tzekova L., Zhou Z., Koop H.-U., 2002, *Plant J.*, in press.

Palmer J. D., *Plastid Chromosomes: Structure and Evolution*, in: Bogorad L. and Vasil I. K. (eds.), *Cell Culture and Somatic Cell Genetics of Plants*, Volume 7A, Academic Press, San Diego, 1991.

The Arabidopsis Genome Initiative, 2000, *Nature*, 408, 796-815.

Svab, Z., Hajdukiewicz, P., and Maliga, P., 1990, *Proc. Natl. Acad. Sci. USA* 87, 8526-8530.

Zhou Z., 2001, PhD thesis, Ludwig-Maximilians-Universität, Munich, Germany.

(US5877402)

(US5451513)

**Claims**

1. A process of generating transgenic plants or plant cells transformed on their plastome, comprising
  - (a) introducing into plant plastids a first DNA molecule and a second DNA molecule, wherein  
said first DNA molecule contains a first region homologous to a region of the plastome for directing plastome integration and a first sequence of interest, and  
said second DNA molecule contains a second region homologous to a region of the plastome for directing plastome integration and a second sequence of interest,  
whereby a sequence segment of said first sequence of interest is homologous to a sequence segment of said second sequence of interest, and
  - (b) selecting transformants having an integration sequence stably integrated in the plastome, whereby said integration sequence contains at least a portion of said first and at least a portion of said second sequence of interest as a continuous sequence.
2. The process of claim 1, wherein said first and said second DNA molecule are introduced into said plant plastids by co-transformation.
3. The process of one of claims 1 or 2, wherein said first and said second sequence of interest are different.
4. The process of one of claims 1 to 3, wherein said first and said second sequence of interest each contains a further sequence in addition to said sequence segment.
5. The process of one of claims 1 to 4, wherein one or more additional DNA molecules are introduced into said plant plastids in addition to said first and said second DNA molecule, whereby said additional DNA molecule(s) comprise(s) additional sequence(s) of interest.

6. The process of claim 5, wherein said one additional DNA molecule contains a sequence segment homologous to a sequence segment of said first sequence of interest and a sequence segment homologous to said second sequence of interest.
7. The process of one of claims 1 to 6, wherein said first and/or said second and/or an additional sequence of interest contains one or more genes of interest or fragments of a gene of interest.
8. The process of one of claims 1 to 7, wherein a gene of interest is split into two or more fragments and wherein said first and/or said second and/or an additional sequence of interest contains a fragment of said gene of interest, whereby said gene of interest is assembled from said two or more fragments upon formation of said integration sequence.
9. The process of one of claims 7 or 8, wherein said gene of interest is a selectable marker gene.
10. The process of one of claims 1 to 9, wherein said first or said second DNA molecule contains a selectable marker gene outside of a sequence unit consisting of the region homologous to a region of the plastome and the sequence of interest, for allowing loss of said marker gene.
11. The process of one of claims 1 to 9, wherein a selectable marker gene is split into a first and a second fragment, whereby said first fragment is incorporated in said first DNA molecule outside of a first sequence unit and said second fragment is incorporated in said second DNA molecule outside of a second sequence unit, whereby said first sequence unit consists of said first homologous region and said first sequence of interest and said second sequence unit consists of said second homologous region and said second sequence of interest.



12. The process of one of one of claims 9 to 11, wherein said selectable marker gene is aphA-6.
13. The process of one of claims 1 to 12, wherein said first DNA molecule contains only one region homologous to a region of the plastome for directing plastome integration.
14. The process of one of claim 1 to 12, wherein said first and said second DNA molecule each contains only one region homologous to a region of the plastome for directing plastome integration.
15. The process of one of claims 1 to 14, wherein said first and said second homologous region together correspond to a continuous sequence of the plastome to be transformed.
16. The process of one of claims 1 to 15, wherein homoplastomic transgenic plants are regenerated from said transformants.
17. Kit-of-parts comprising a first and a second DNA molecule as defined in one of claims 1 to 16.
18. DNA molecule for plastid transformation containing one region homologous to a region of a plastome for directing plastome integration and a sequence of interest.
19. Library of DNA molecules according to claim 18, whereby each of said DNA molecules contains a different sequence of interest.
20. Plant or plant cells transformed with said DNA molecules of said kit of claim 17 or with said DNA molecule of claim 18.
21. Plant, plant cell or seeds obtained according to the process of one of claims 1 to 16.

**Abstract**

A process of generating transgenic plants or plant cells transformed on their plastome, comprising

- (a) introducing into plant plastids a first DNA molecule and a second DNA molecule, wherein  
said first DNA molecule contains a first region homologous to a region of the plastome for directing plastome integration and a first sequence of interest, and  
said second DNA molecule contains a second region homologous to a region of the plastome for directing plastome integration and a second sequence of interest, whereby a sequence segment of said first sequence of interest is homologous to a sequence segment of said second sequence of interest, and
- (b) selecting transformants having an integration sequence stably integrated in the plastome, whereby said integration sequence contains at least a portion of said first and at least a portion of said second sequence of interest as a continuous sequence.

1/10

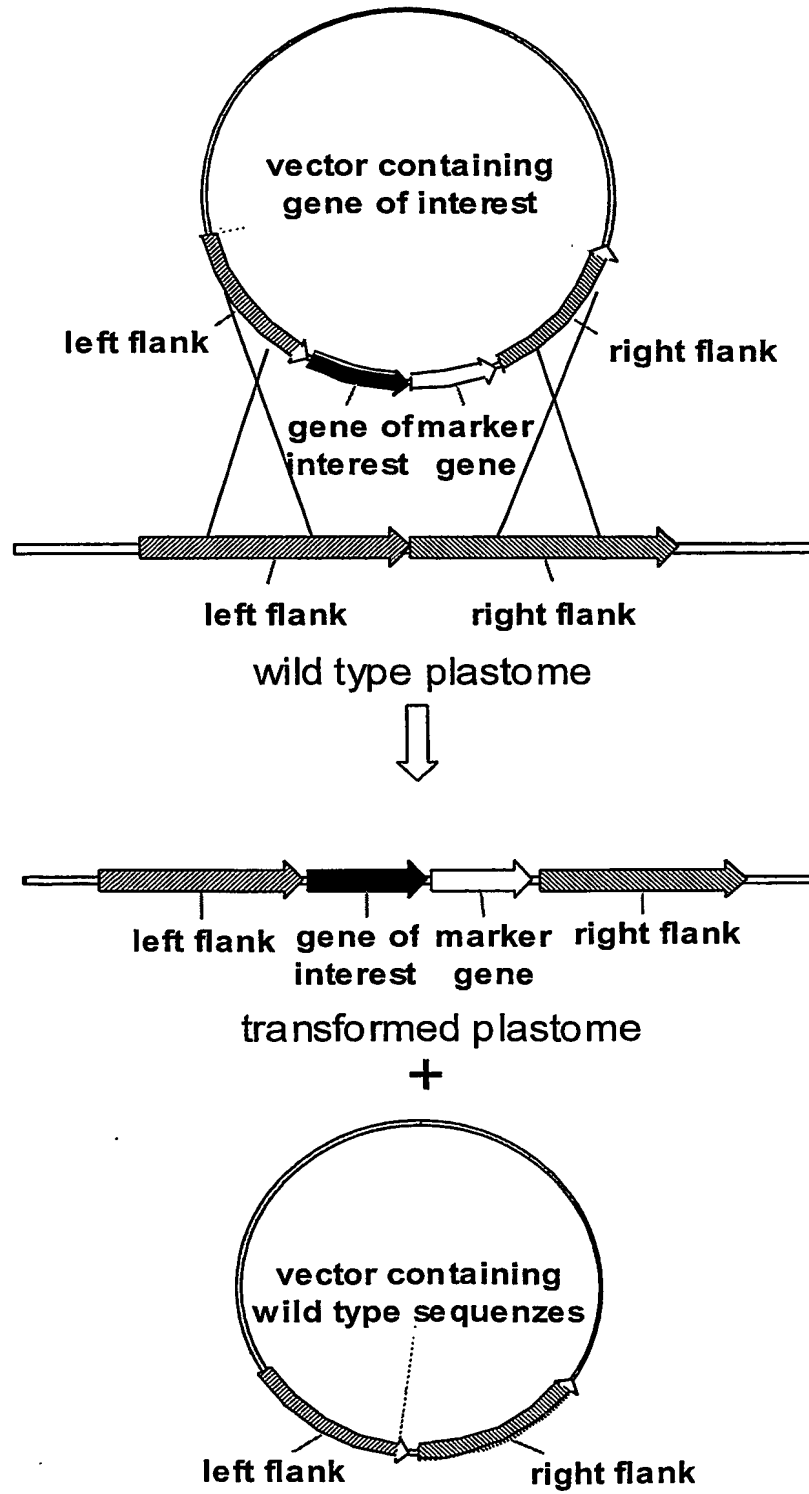


Fig. 1

2/10

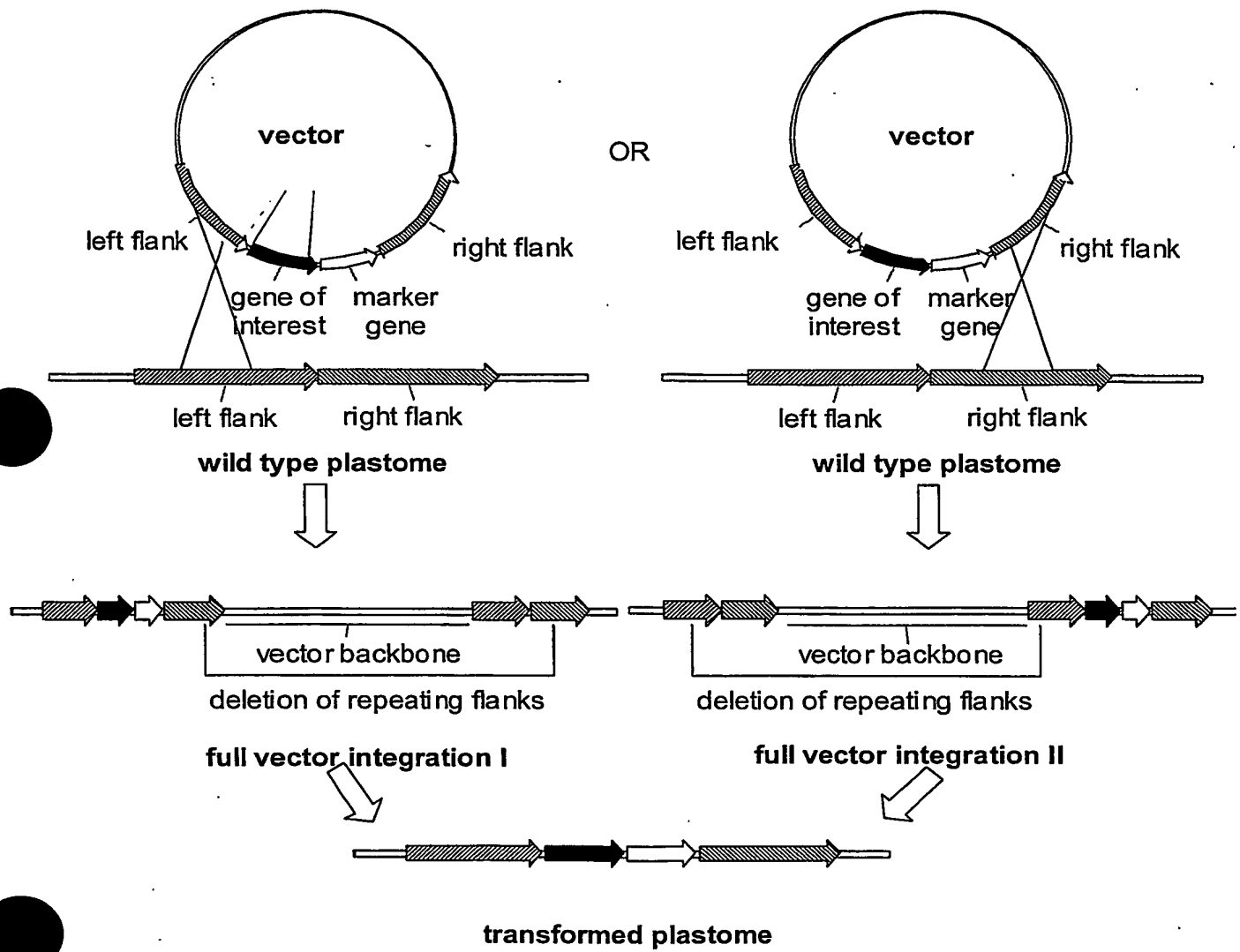


Fig. 2

3/10

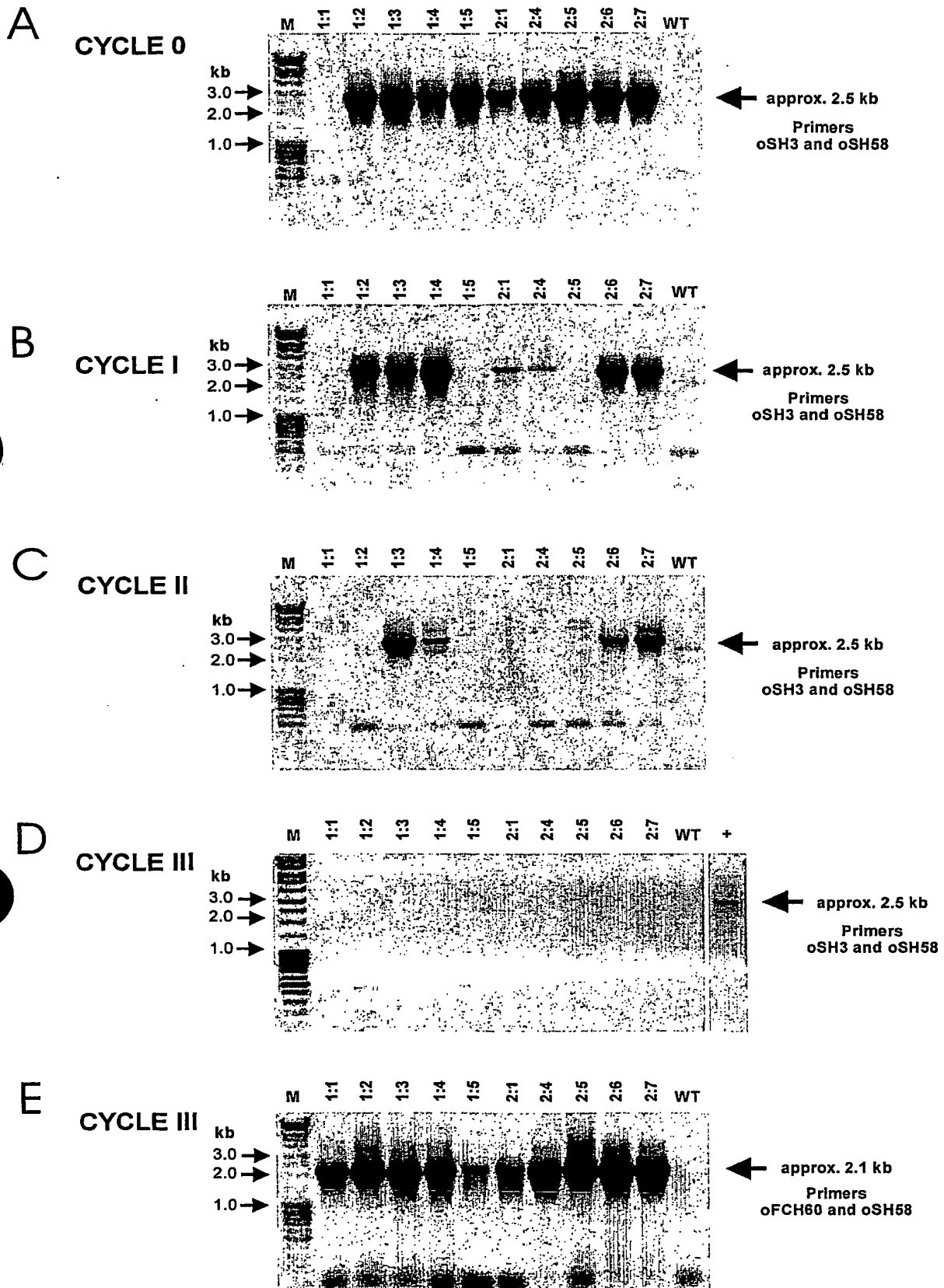


Fig. 3

4/10

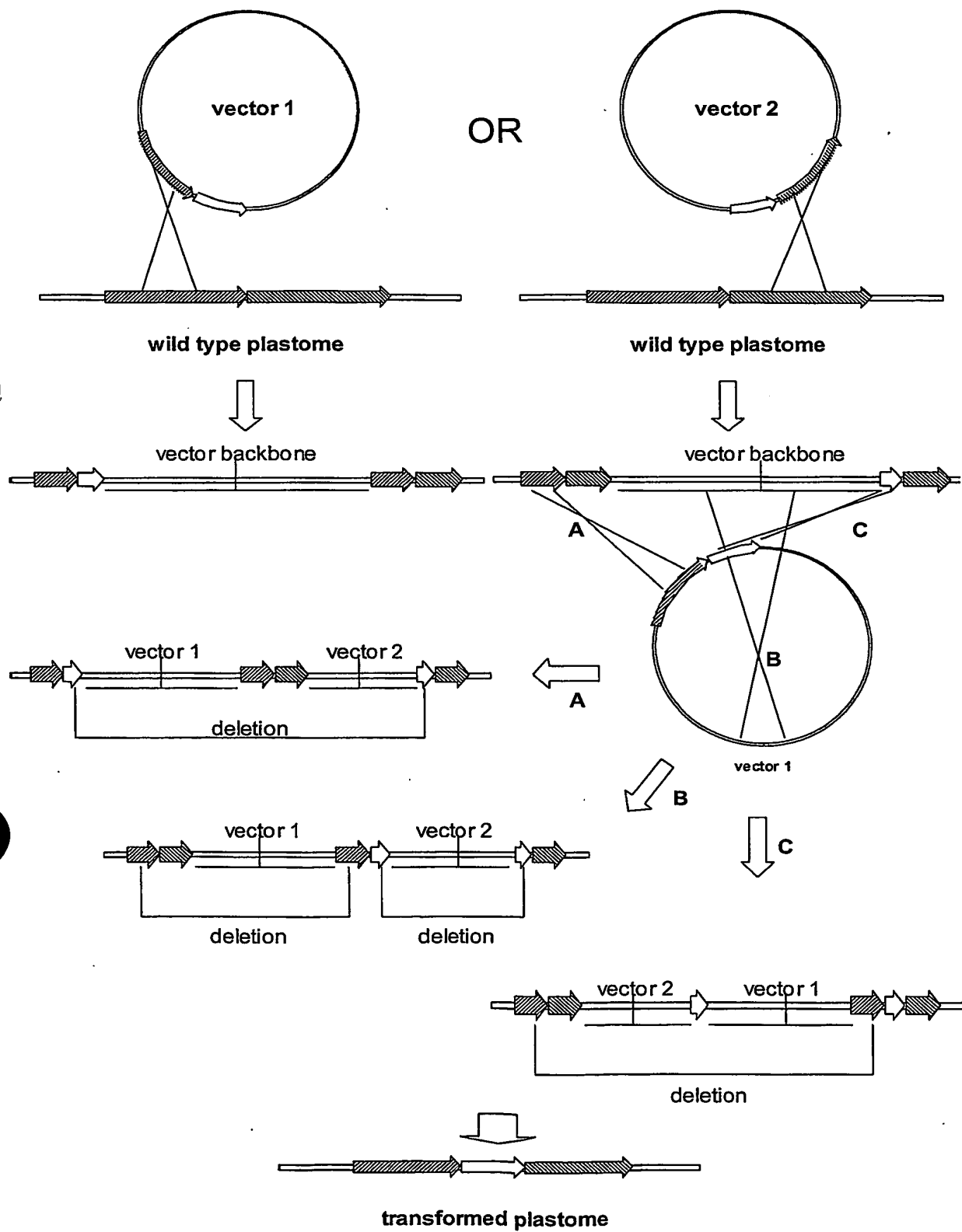


Fig. 4

5/10

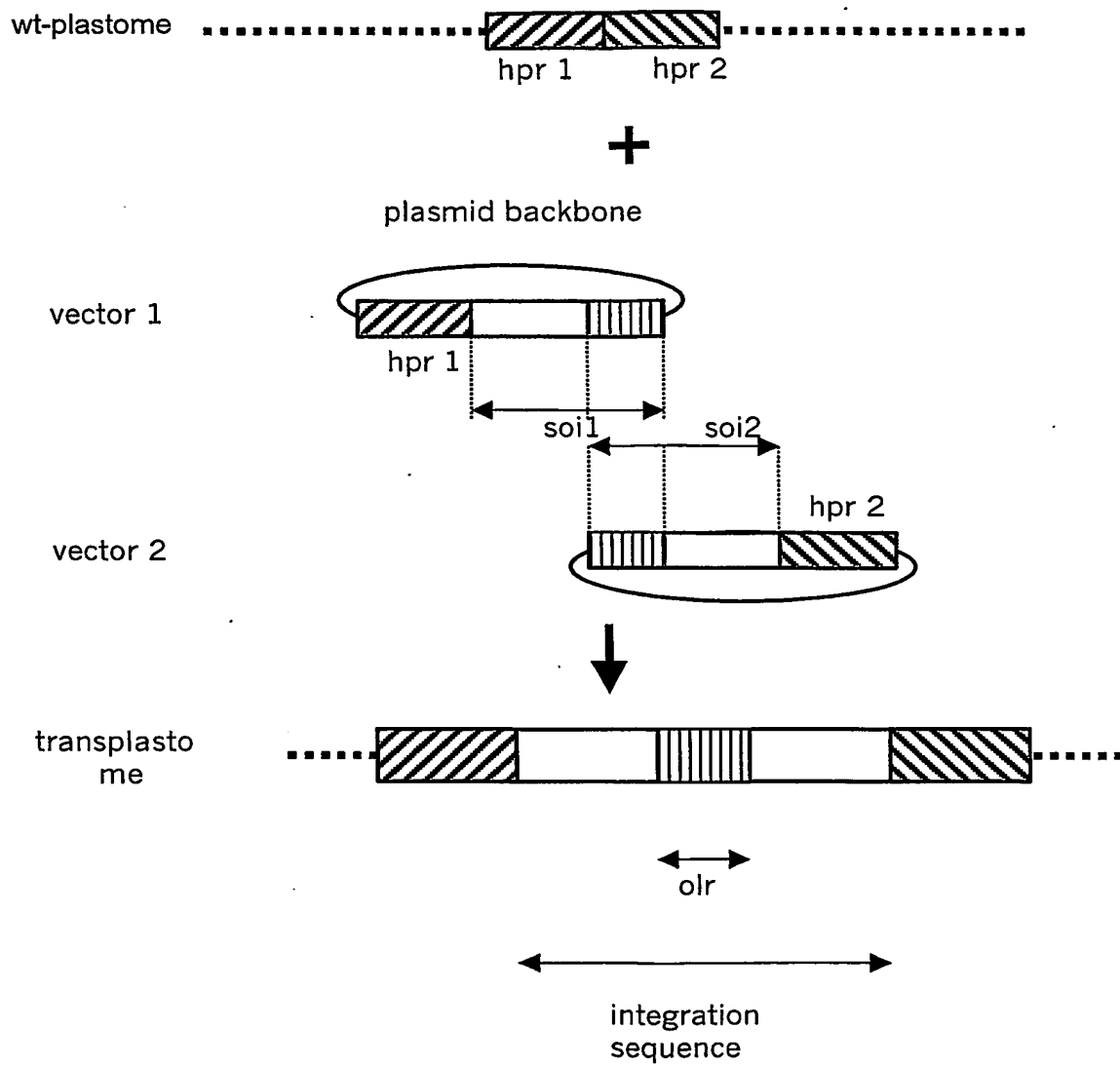


Fig. 5

6/10

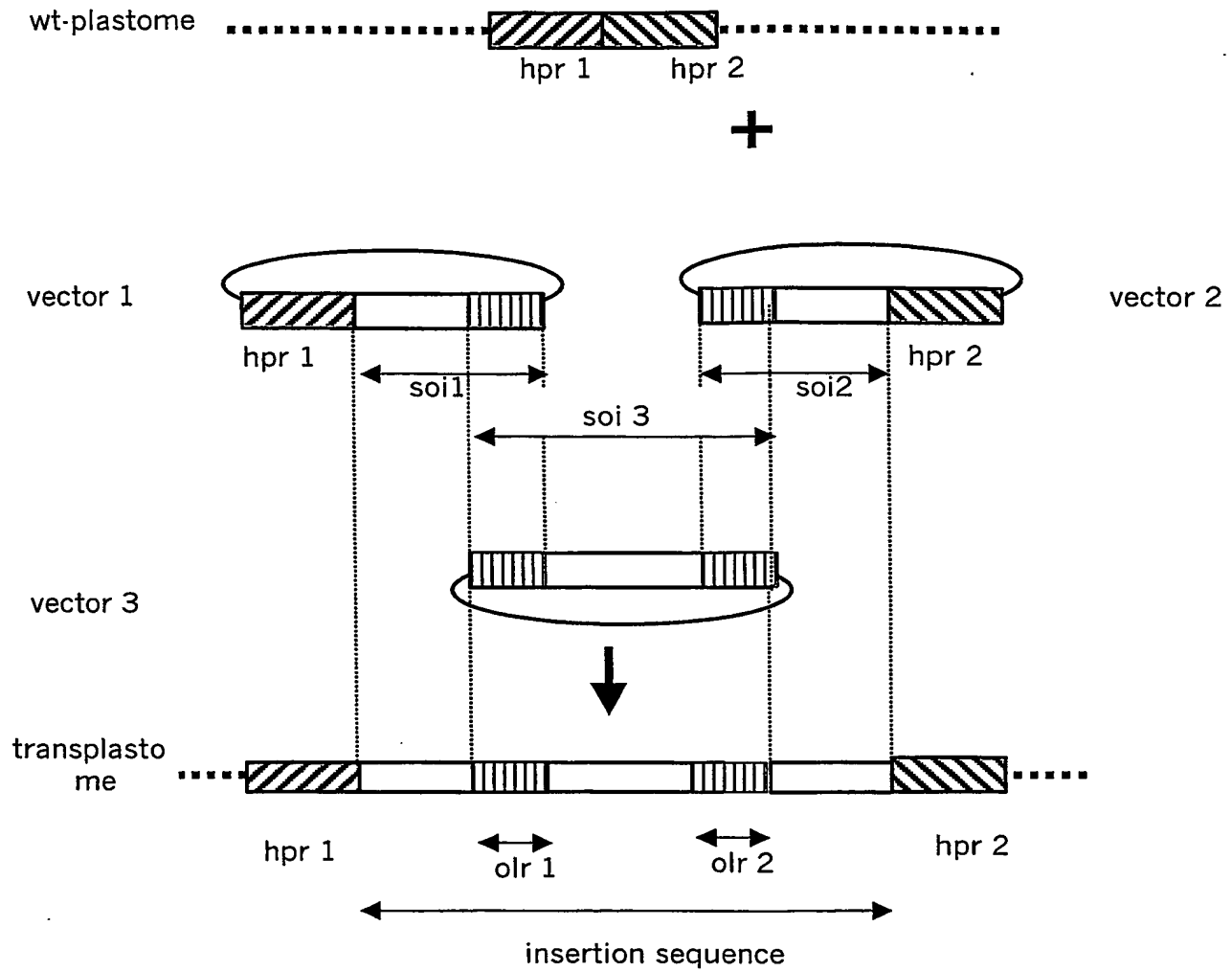


Fig. 6



7/10

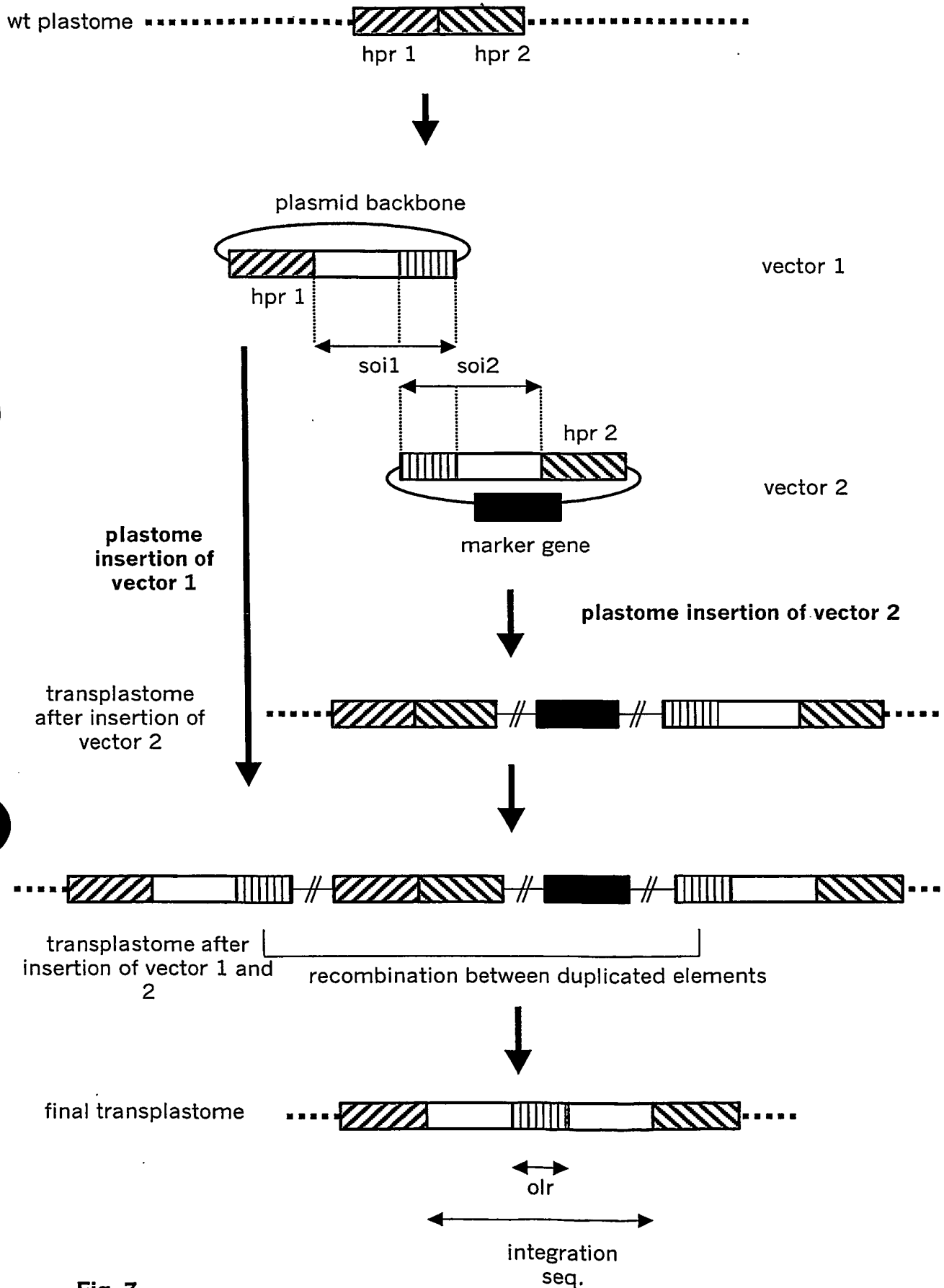


Fig. 7

8/10

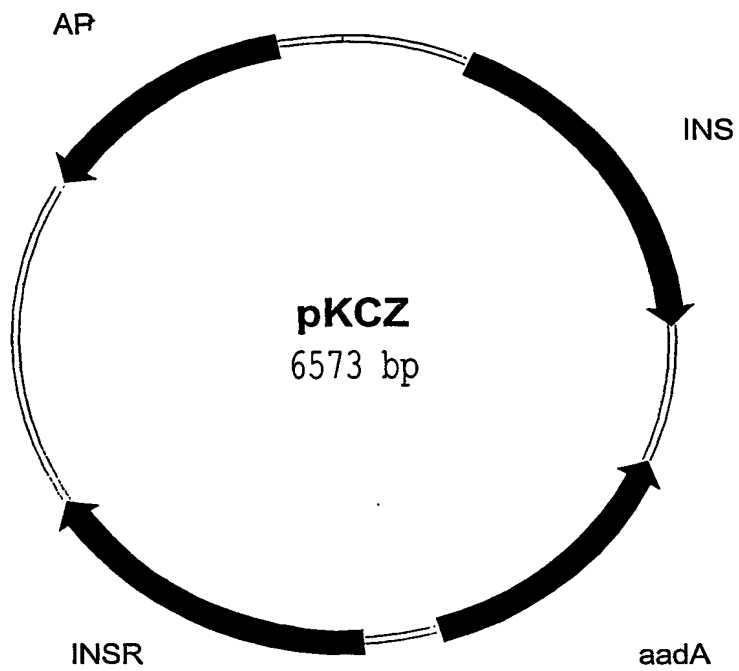


Fig. 8

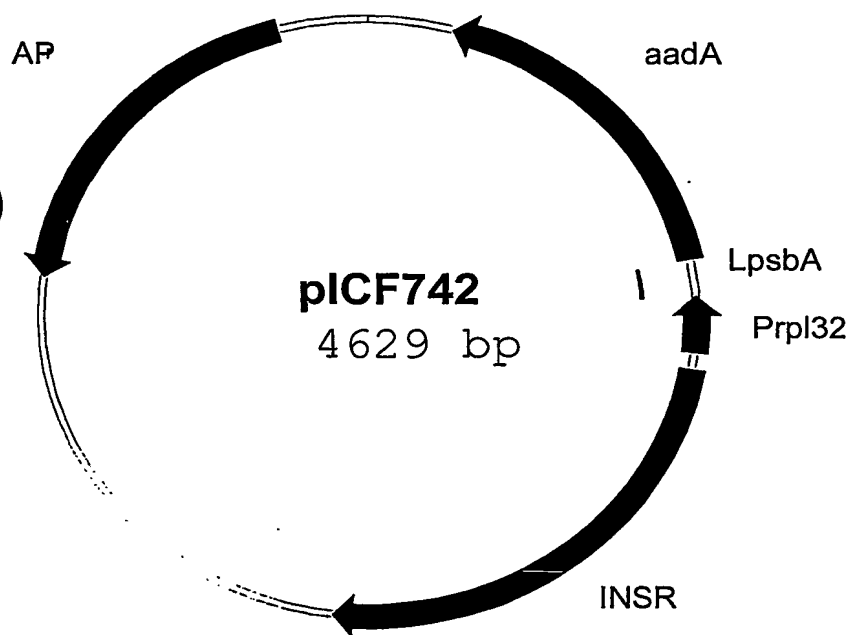


Fig. 9

9/10

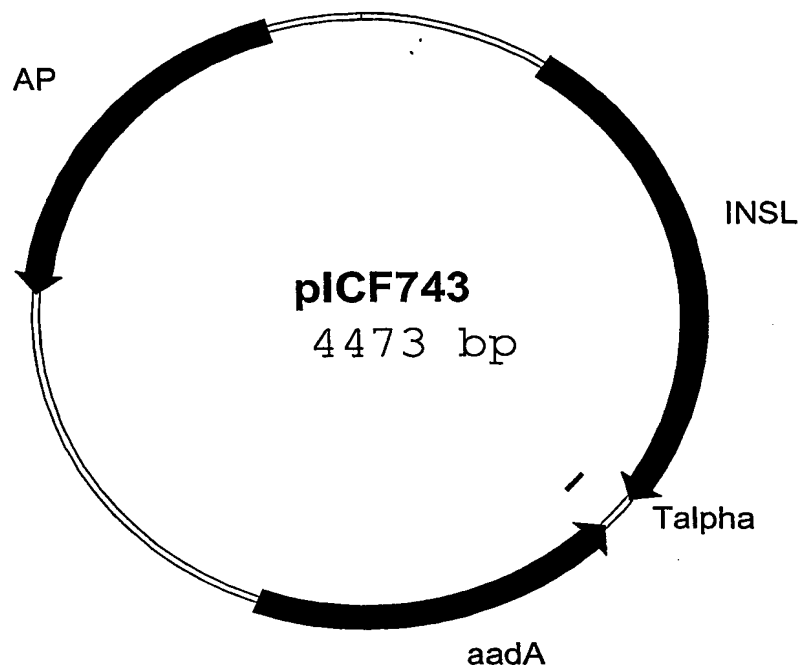


Fig. 10

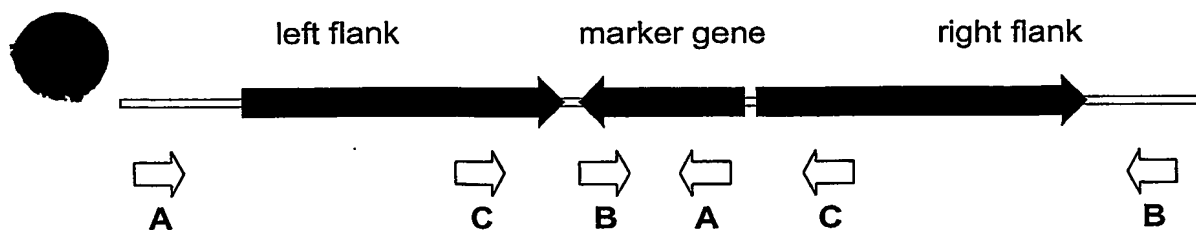


Fig. 11

10/10

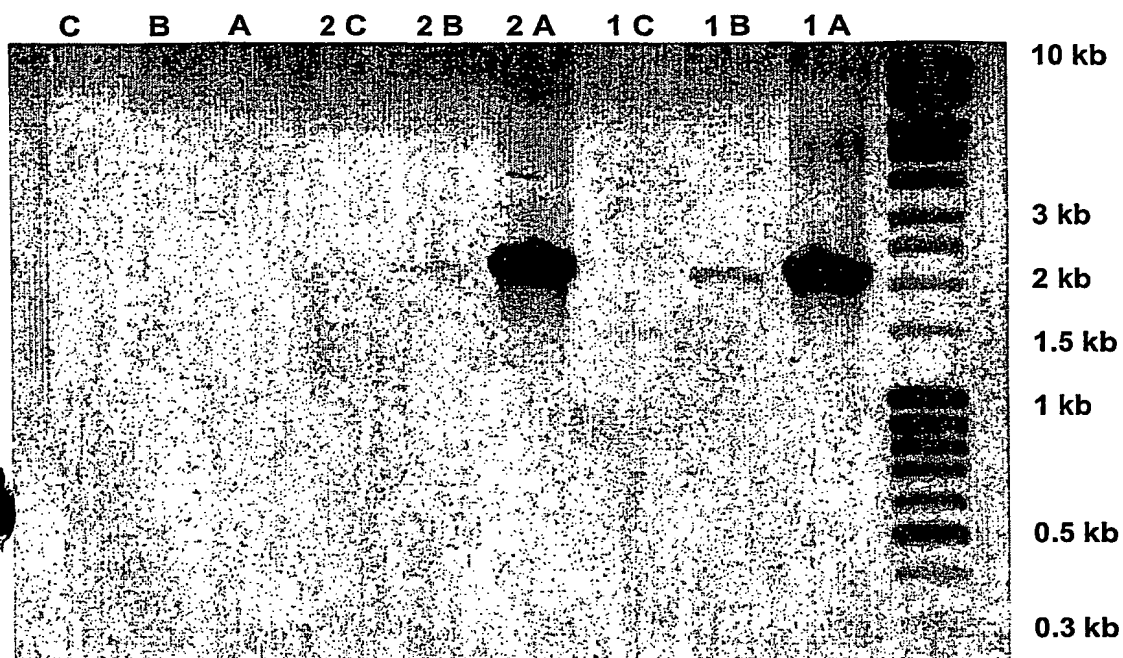


Fig. 12

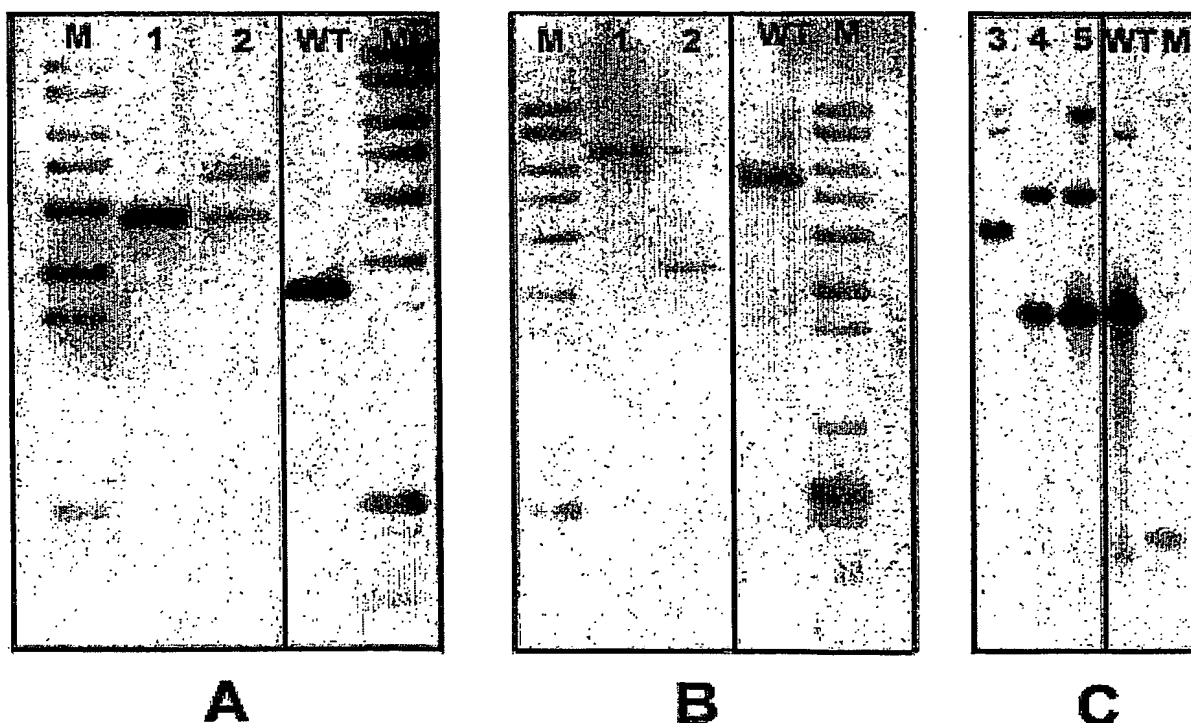


Fig. 13

**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

☐ **BLACK BORDERS**

☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**

☒ **FADED TEXT OR DRAWING**

☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**

☐ **SKEWED/SLANTED IMAGES**

☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**

☐ **GRAY SCALE DOCUMENTS**

☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**

☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**

☐ **OTHER:** \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**